# $\underline{\mathsf{BLAST}}^{\textcircled{\$}} \Rightarrow \underline{\mathsf{blastn suite}} \Rightarrow \mathsf{results} \ \mathsf{for} \ \mathsf{RID-S4KEEF97015}$

Job Title <u>Nucleotide Sequence ...</u>

RID <u>S4KEEF97015</u> Search expires on 09-19 23:31 pm

Program BLASTN

Database nr

Description None ...

Molecule type dna

Query Length 1092

#### **Descriptions**

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1858	1858	93%	0.0	99.42%	AK154309.1
PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1740	1740	93%	0.0	97.56%	XM_006510253.2
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic	1740	1882	93%	0.0	97.56%	JN961338.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgu; transgenic	1740	1882	93%	0.0	97.56%	<u>JN951773.1</u>
Mus musculus sterol-C5-desaturase (Sc5d), mRNA	1740	1740	93%	0.0	97.56%	NM_172769.2
Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence	1740	1992	93%	0.0	97.56%	AC160051.2
Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1740	1740	93%	0.0	97.56%	AK077670.1
Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1740	1740	93%	0.0	97.56%	AK043825.1
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA	1576	1576	93%	0.0	94.63%	XM_029481771.1
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	1576	1576	93%	0.0	94.63%	XM_021172472.2
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1576	1576	93%	0.0	94.63%	XM_021172471.1

12	.019	NCBI Blast. Nucleotide Sequence						
	Description	Max	Total	Query	E	Per.	Accession	
		Score	Score	Cover	value	Ident		
	PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1103	1103	91%	0.0	87.55%	XM 021207205.2	
	Mus musculus C5D mRNA for sterol-C5- desaturase, complete cds	979	979	49%	0.0	99.44%	AB016248.1	
	Mus musculus sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), mRNA (cDNA clone MGC:37898 IMAGE:5101986), complete cds	977	977	48%	0.0	100.00%	BC024132.1	
	PREDICTED: Rattus norvegicus sterol- C5-desaturase (Sc5d), transcript variant X1, mRNA	749	749	91%	0.0	81.24%	XM_017595406.1	
	Rattus norvegicus sterol-C5-desaturase (Sc5d), mRNA	749	749	91%	0.0	81.24%	NM_053642.2	
	Mus musculus BAC clone RP23-346J12 from chromosome 6, complete sequence	702	792	56%	0.0	90.04%	AC122333.2	
	PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	699	699	57%	0.0	87.84%	XM_021207206.2	
	Mus musculus predicted gene, 31520 (Gm31520), non-coding RNA	678	678	48%	0.0	89.80%	NR_136927.1	
	Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830041I17 product:weakly similar to STEROL C5-DESATURASE [Rattus norvegicus], full insert sequence	678	678	48%	0.0	89.80%	AK052921.1	
	PREDICTED: Mus pahari lathosterol oxidase-like (LOC110334695), mRNA	579	579	49%	1e-160	87.25%	XM_029547953.1	
	PREDICTED: Mesocricetus auratus sterol-C5-desaturase (Sc5d), mRNA	424	678	77%	6e-114	79.62%	XM_005069403.3	
	Rattus norvegicus C5D mRNA for sterol C5-desaturase, complete cds	407	407	47%	6e-109	81.46%	AB052846.1	
	PREDICTED: Cricetulus griseus sterol- C5-desaturase (Sc5d), transcript variant X2, mRNA	396	396	53%	1e-105	79.44%	XM_007651891.3	
	PREDICTED: Cricetulus griseus sterol- C5-desaturase (Sc5d), transcript variant X1, mRNA	396	396	53%	1e-105	79.44%	XM_003511371.4	
	PREDICTED: Cricetulus griseus sterol- C5-desaturase (Sc5d), transcript variant X2, mRNA	392	392	53%	2e-104	79.30%	XM_027411877.1	
	PREDICTED: Cricetulus griseus sterol- C5-desaturase (Sc5d), transcript variant X1, mRNA	392	392	53%	2e-104	79.30%	XM_027411876.1	
	Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330029P19 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	311	311	16%	5e-80	97.79%	AK165139.1	
	Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730048E03 product:unclassifiable, full insert sequence	292	292	16%	2e-74	96.61%	AK050439.1	
	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Cd3eap:tm1a(KOMP)Wtsi; transgenic	185	303	11%	3e-42	93.65%	JN957866.1	

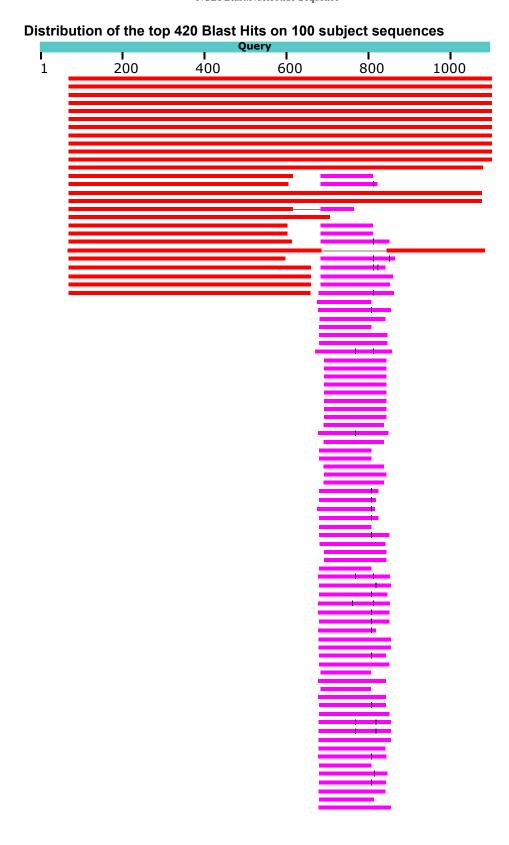
5/ ZC	019	NCBI Biast: Nucleotide Sequence							
	Description	Max	Total	Query	Е	Per.	Accession		
	·	Score	Score	Cover	value	Ident			
	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ercc1:tm1a(KOMP)Wtsi tm2a(KOMP)Wtsi; transgenic	185	394	11%	3e-42	93.65%	JN955142.1		
	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Cd3eap:tm1e(KOMP)Wtsi; transgenic	185	303	11%	3e-42	93.65%	JN949926.1		
	Mus musculus CD3E antigen, epsilon polypeptide associated protein (Cd3eap), mRNA	185	185	11%	3e-42	93.65%	NM 145822.2		
	Mus musculus chromosome 7, clone RP23-457C1, complete sequence	185	1735	14%	3e-42	93.65%	AC118017.15		
	Mus musculus BAC clone RP23-152A3 from chromosome 9, complete sequence	185	1367	15%	3e-42	88.12%	AC159821.2		
	Mus musculus BAC clone RP23-85B15 from chromosome 7, complete sequence	185	1346	13%	3e-42	93.65%	AC148988.5		
	Mus musculus BAC clone RP23-135K11 from chromosome 8, complete sequence	183	2499	15%	1e-41	86.78%	AC163625.5		
	Mus musculus strain C57BL/6J chromosome 8 clone rp23-340n2, complete sequence	183	1760	14%	1e-41	86.78%	AC093451.25		
	Mus musculus chromosome 12, clone RP24-276C17, complete sequence	182	1209	15%	4e-41	92.91%	AC115037.16		
	Mus musculus BAC clone RP24-140F3 from 12, complete sequence	182	921	11%	4e-41	92.91%	AC117240.4		
	Mus musculus BAC clone RP23-322K1 from chromosome 14, complete sequence	180	1311	15%	1e-40	92.31%	AC125180.6		
	Mus musculus BAC clone RP23-240E9 from chromosome 9, complete sequence	180	728	14%	1e-40	87.50%	AC160392.2		
	Mus musculus CD3E antigen, epsilon polypeptide associated protein, mRNA (cDNA clone MGC:78047 IMAGE:6478245), complete cds	180	180	11%	1e-40	92.80%	BC071199.1		
	Mus musculus BAC clone RP23-358C4 from chromosome 9, complete sequence	178	178	14%	5e-40	86.39%	AC183268.4		
	Mus musculus BAC clone RP23-408I18 from chromosome 9, complete sequence	178	178	14%	5e-40	86.39%	AC153009.4		
	Mouse DNA sequence from clone RP23- 253E9 on chromosome 11, complete sequence	178	3465	15%	5e-40	86.39%	AL591113.14		
	PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X8, mRNA	176	176	13%	2e-39	88.16%	XM_030252585.1		
	PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X7, mRNA	176	176	13%	2e-39	88.16%	XM_030252584.1		
	PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X6, mRNA	176	176	13%	2e-39	88.16%	XM_017319548.2		
	PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X5, mRNA	176	176	13%	2e-39	88.16%	XM_006501389.4		
	PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X4, mRNA	176	176	13%	2e-39	88.16%	XM_017319547.1		

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Description	Max	Total	Query	Е	Per.	Accession
·	Score	Score	Cover	value	Ident	
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X3, mRNA	176	176	13%	2e-39	88.16%	XM_017319546.1
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X2, mRNA	176	176	13%	2e-39	88.16%	XM_006501386.3
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X1, mRNA	176	176	13%	2e-39	88.16%	XM 006501385.3
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Defb22:tm1a(KOMP)Wtsi; transgenic	176	176	13%	2e-39	89.12%	JN963878.1
Mus musculus targeted deletion, lacZ- tagged mutant allele Sf3b4:tm1(KOMP)Ucd; transgenic	176	292	14%	2e-39	88.16%	JN960976.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Defb26:tm1a(KOMP)Wtsi; transgenic	176	176	13%	2e-39	89.12%	<u>JN959925.1</u>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele 9130017N09Rik:tm2e(EUCOMM)Wtsi tm1e(EUCOMM)Wtsi; transgenic	176	534	11%	2e-39	92.13%	JN958274.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele 9130017N09Rik:tm2a(EUCOMM)Wtsi; transgenic	176	534	11%	2e-39	92.13%	JN958273.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Defb26:tm1e(KOMP)Wtsi; transgenic	176	176	13%	2e-39	89.12%	JN956718.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Otud7b:tm1a(EUCOMM)Wtsi; transgenic	176	343	13%	2e-39	88.16%	JN952505.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Defb22:tm1e(KOMP)Wtsi; transgenic	176	176	13%	2e-39	89.12%	JN948829.1
Mus musculus BAC clone RP23-13B8 from chromosome 10, complete sequence	176	2625	11%	2e-39	92.13%	AC151846.3
Mus musculus chromosome 15, clone RP23-195I24, complete sequence	176	503	11%	2e-39	92.19%	AC161812.3
Mus musculus chromosome 1, clone RP24-400M20, complete sequence	176	817	11%	2e-39	92.13%	AC116853.12
Mus musculus BAC clone RP24-389C22 from chromosome 10, complete sequence	176	1627	11%	2e-39	92.13%	AC124407.4
Mus musculus chromosome 15, clone RP24-366J14, complete sequence	176	853	11%	2e-39	92.19%	AC163018.3
Mus musculus chromosome 2 clone RP23-286D16, complete sequence	176	685	14%	2e-39	87.12%	AC019153.13
Mouse DNA sequence from clone RP23- 332C5 on chromosome 11, complete sequence	176	290	14%	2e-39	87.20%	AL645738.14
Mus musculus OTU domain containing 7B (Otud7b), transcript variant 1, mRNA	176	176	13%	2e-39	88.16%	NM 001025613.1
Mus musculus OTU domain containing 7B (Otud7b), transcript variant 2, mRNA	176	176	13%	2e-39	88.16%	NM 001025614.1
Mus musculus BAC clone RP23-138K22 from 9, complete sequence	176	1679	11%	2e-39	92.13%	AC140409.3

5/ 2	019	INCBI Biast: Nucleotide Sequence						
	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession	
	Mus musculus BAC clone RP24-201C14 from 3, complete sequence	176	739	14%	2e-39	88.16%	AC125099.3	
	Mouse DNA sequence from clone RP23- 453K8 on chromosome 2, complete sequence	176	499	15%	2e-39	87.42%	AL844517.6	
	Mouse DNA sequence from clone RP23- 188D9 on chromosome 2, complete sequence	176	685	14%	2e-39	87.50%	BX004793.12	
	Mus musculus strain C57BL/6J chromosome 3 clone rp23-261m19, complete sequence	176	803	14%	2e-39	88.16%	AC092094.19	
	Mouse DNA sequence from clone RP23- 391H10 on chromosome 2, complete sequence	176	1193	15%	2e-39	92.19%	AL805959.11	
	Mouse DNA sequence from clone RP23- 120N11 on chromosome 4, complete sequence	176	1727	14%	2e-39	92.13%	AL683890.7	
	Mouse DNA sequence from clone RP23- 129N7 on chromosome 5, complete sequence	176	1345	11%	2e-39	91.54%	AL513345.20	
	Mus musculus FtsJ RNA methyltransferase homolog 1 (E. coli) (Ftsj1), transcript variant 2, mRNA	174	174	15%	6e-39	85.23%	NM_001290430.1	
	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ftsj1:tm1e(EUCOMM)Wtsi; transgenic	174	433	15%	6e-39	85.23%	JN961376.1	
	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Fbxo17:tm1e(EUCOMM)Wtsi; transgenic	174	613	14%	6e-39	87.04%	JN957410.1	
	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Rnd1:tm1a(EUCOMM)Wtsi; transgenic	174	303	15%	6e-39	85.71%	JN954778.1	
	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Micall2:tm1e(KOMP)Wtsi; transgenic	174	288	10%	6e-39	92.68%	JN954776.1	
	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Hnrnpu:tm1e(EUCOMM)Wtsi; transgenic	174	174	14%	6e-39	86.31%	JN953467.1	
	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Micall2:tm1a(KOMP)Wtsi; transgenic	174	288	10%	6e-39	92.68%	JN950802.1	
	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Hnrnpu:tm1a(EUCOMM)Wtsi; transgenic	174	174	14%	6e-39	86.31%	JN949506.1	
	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Fbxo17:tm1a(EUCOMM)Wtsi; transgenic	174	613	14%	6e-39	87.04%	JN949490.1	
	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Rnd1:tm1e(EUCOMM)Wtsi; transgenic	174	303	15%	6e-39	85.71%	JN947814.1	
	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ywhaq:tm1e(EUCOMM)Hmgu; transgenic	174	418	14%	6e-39	90.91%	JN947747.1	

	Nebi Biast. Autocolde Sequence					
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ywhaq:tm1a(EUCOMM)Hmgu; transgenic	174	418	14%	6e-39	90.91%	<u>JN947251.1</u>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ftsj1:tm1a(EUCOMM)Wtsi; transgenic	174	433	15%	6e-39	85.23%	JN945613.1
Mus musculus chromosome 1, clone RP24-252K15, complete sequence	174	1034	14%	6e-39	86.67%	AC166710.7
Mus musculus BAC clone RP23-27C10 from chromosome 1, complete sequence	174	1055	14%	6e-39	86.67%	AC125377.5
Mus musculus BAC clone RP23-264L8 from chromosome 14, complete sequence	174	844	11%	6e-39	92.06%	AC158983.2
Mus musculus BAC clone RP23-168E11 from chromosome 5, complete sequence	174	1239	13%	6e-39	92.68%	AC130221.4
Mus musculus BAC clone RP24-505G5 from chromosome 7, complete sequence	174	376	14%	6e-39	88.51%	AC125372.4
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832403P19 product:DSCAM- interacting protein 1 homolog [Mus musculus], full insert sequence	174	174	14%	6e-39	86.50%	AK161178.1
Mus musculus BAC clone RP24-490B17 from chromosome 17, complete sequence	174	174	11%	6e-39	90.91%	AC154796.2
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630055M22 product:Ftsj homolog (E. coli), full insert sequence	174	174	15%	6e-39	85.23%	AK036313.1

#### **Graphic Summary**



# Alignments

Alignment view Pairwise 

CDS feature

Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence

Sequence ID: AK154309.1 Length: 2251 Number of Matches: 1

Range 1: 1101 to 2127

Score Expect Identities Gaps Strand Frame

			NCBI Biast.Nuci	eonde Sequence	
s(1006)	0.0()	1021/1027(99%)	5/1027(0%)	Plus/Plus	
71	GTGGTGCCATT	rggaatgtcagcattgc	TTGAGTGTCATGCTC	GAGGGATGGTCCTGACAGT	130
1101	ĠŦĠĠŦĠĊĊĂŦŢ	rggaatgtcagcattgc	cttgagtgtcatgctd	SAGGGATGGTCCTGACAGT	1160
131	AAACAGCGGGA	AAGACACCAGGAGCATT	GTAATCGCTTGGTTA	ATTGTCCGACATTGGTCC	190
1161	AAAĊAĠĊĠĠĠ <i>I</i>	A A G A C A C C A G G A G C A T T	ŗĠŦÀÀŦĊĠĊŦŦĠĠŦŦĀ	AATTĠŦĊĊĠĀĊĀŦŦĠĠŦĊĊ	1220
191	AGGAACAACTT	FGTCTTTTCAGCCGGCT 	GACCTGCAGCCTGT <i>F</i>	ACAGCTCTGAAGCATCTTT	250
1221	ÀĠĠÀĀĊĀĀĊŤ'	rĠŦĊŦŦŦŦĊĀĠĊĊĠĠĊŦ	ĠĀĊĊŦĠĊĀĠĊĊŦĠŦĀ	\CAĠĊŤĊŤĠAĀĠĊĀŤĊŤŤŤ	1280
251					310
					1340
					370
					1400
					430 1460
					490
1461					1520
491	ŢĢĢĄŢĄĢĢĄŢ	ӷҭҫҪҭҭѧѧҭҫҫҪҭҫѧҭҫ	; ;таатаа <u>датт</u> дтаст	ŢŢĊĊŢĄŢĄĊĄĠĄĠĠĊĄĊĊŢ	550
1521	 TGGATAGGAT				1580
551	TACTCTCTGGG	GGCATTATCAGATTTTA	ATAAATGAATAAAT	AATGGTAttttttAAA	610
1581	TACTCTCTGG			AATGGTATTTTTTTAAA	1640
611	TGTCAGCTCT	CCATAATTCAGTCTAG	ATAGGAGATTATTTA	AACTGAAGATCTCTTGGTG	670
1641	TGTCAGCTCT:	rccataattcagtctad	sataggagattattt	Actgaagatctcttggtg	1700
671	AGTGTCAttt	tttttctttct	:tttttttttttttt	tttggttttttAAGACAG	725
1701					1760
					785
					1820
					845
					1880 905
					1940
					965
					2000
966					1025
2001	 TCTCAGTTAC		 TGAAGGGATAAT		2060
1026	ÇÇŢĄĄĢĢŢĄÇ	АСТТТАGАССТСАТСТТ	СТАТТТСТТСССТСТ	ССТТСТССАААТСААСААА	1085
2061	CCTAAGGTAC				2120
1086	ACAAAAC 10	92			
2121	ACAAAAC 2	127			
	71 1101 131 1161 191 1221 251 1281 311 1341 371 1401 431 1461 491 1521 551 1581 611 1641 671 1701 726 1761 786 1821 846 1881 906 1941 966 2001 1026 2061 1086	71 GTGGTGCCATT 1101 GTGGTGCCATT 131 AAACAGCGGGA 1161 AAACAGCGGGA 1161 AAACAGCGGGA 1161 AAACAGCGGGA 191 AGGAACAACTT 1221 AGGAACAACTT 1221 AGGAACAACTT 1221 AGGAACAACTT 1341 GCATACTCATT 1341 GCATACTCATT 1341 GCATACTCATT 1341 GCATACTCATT 1341 GCATACTCATT 1341 GTGCAGGACT 1401 ACCCTAAAGAT 1401 ACCCTAAAGAT 1401 ACCCTAAAGAT 1521 TGGATAGGAT 1521 TGGATAGGAT 1521 TGGATAGGAT 1521 TGGATAGGAT 1531 TACTCTCTGGC 1581 TACTCTCTGGC 111 TGTCAGCTCTT 1641 TGTCAGCTCTT 1641 TGTCAGCTCTT 1761 GGTTTCTCTGT 1761 GGTTCATTTAT 1881 GTGTCATTTAT	GTGGTGCCATTGGAATGTCAGCATTGC  1101 GTGGTGCCATTGGAATGTCAGCATTGC  131 AAACAGCGGGAAGACACCAGGAGCATT  1161 AAACAGCGGGAAGACACCAGGAGCATT  191 AGGAACAACTTGTCTTTTCAGCCGGCT  1221 AGGAACAACTTGTCTTTTCAGCCGGCT  1221 AAATACGATAGAAAATAAGTTACTCAA  1161 AAACAGCGATAGAAAATAAGTTACTCAA  1281 AAATACGATAGAAAATAAGTTACTCAA  1341 GCATACTCATTAAGGAAAAATAAGTTACTCAA  1341 GCATACTCATTAAGGAAAAAAAAAAGTACC  1341 GCATACTCATTAAGGAAAAAAAAAAAAAAAAAAAAAAAA	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTC TGTGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTC TGTGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTC TGTGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTC TGTGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTC TGTGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTC TGTGTGCCATTGGAATGTCAGCATTGTAATCGCTTGGTTA T161  AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTA T161  AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTA T161  AAGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTA T161  AAGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTA T161  AAATACGATAGAAAATAAGCTTACTCAAGAAGCTGGTCTGTGT T161  AAATACGATAGAAAAATAAGCTACTCAAGAAGCTGGTCTGTGT T161  GCATACTCATTAAGGAAAAAAAAAGTACCATTGTGCTAAAACGCT TACCCTAAAAGATGAAAAAAAAAA	GONE 1021/1027(99%) 5/1027(0%) PIUS/PIUS  TI GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT  1101 GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT  1101 GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT  111 AAACAGCGGGAAGCACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTC  1161 AAACAGCGGGAAGCACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTC  117 AGGAACAACTTGTCTTTTCAGCCGGGTGACTGCAGCCTGTACAGCTCTGAAGCATCTTT  1221 AGGAACAACTTGTCTTTTCAGCCGGGTGACTGCAGCCTGTACAGCTCTGAAGCATCTTT  1231 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTTCCCTTTGCCTTTAGCCTATGTCCAT  1281 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTTAGCCCT  1281 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTTAGCCCTAG  1311 GCATACTCATTAAGGGAAAAAAAATACCATTGTGCTAAAGCGTACTGGAGCATAACCAGGAA  1312 GCATACTCATTAAGGGAAAAAAAATCCATTGTGCTAAAGCGTACTGGAGCATAACCAGGAA  1313 GCATACTCATTAAGGAAAAAAAATTCCGTCCCCGGAGCGGTGGTCCACCGCAGTGCTGGGA  1314 GCATACTCATTAAGGAAAAAAAATACCATTGTGCTAAAGCCTACTGGAGCTAACCAGGAA  1316 GCATACTCATTAAGGAAAAAAAATACCATTGTCCAAGCAGCTACTGGAGCTAACCAGGAA  1317 ACCCTAAAGATGAAGAATTTCCTGTCCCCGGAGCGGCTGGTCCACCGCAGTGCTGGGGA  1318 GTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGCTCCACCGCAGTGCTGGGAA  1319 GTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGCCAG  1320 TGGAAGGATTTCCTTAATGGCTGATGTAATAACAATTGTACTTCCTTATACAGAGGCACCT  1321 TGGAAGGATTTCCTTAATGGCTGATGTAATAACAATTGTACTTCCTTATACAGAGGCACCT  1321 TGGAAGGATTTCCTTAATGGCTGATGTAATAACAATTGTACTTCCTTATACAGAGGCACCT  1321 TGCAGGACTTCCATAATTCAGGTTATATAAAATAAAATA

PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA

Sequence ID: XM\_006510253.2 Length: 4826 Number of Matches: 1

Range 1: 1146 to 2158

Score		Expect	Identities	Gaps	Strand	Frame	
1740 bits	s(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus		
Query	71	GTGGTGCCAT	TGGAATGTCAGCATTG	CTTGAGTGTCATGCT	GAGGGATGGTC	CTGACAGT	130

3/2019		NCBI Blast:Nucleotide Sequence	
Sbjct	1146	$\tt GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT$	1205
Query	131	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	190
Sbjct	1206	AAACAGCGGGAAGACACCGGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	1265
Query	191	AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	250
Sbjct	1266	AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	1325
Query	251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT	310
Sbjct	1326	aaatacgatagaaaataagctactcaagaagctgcttgtgtgtccttttgcctttagtccat	1385
Query	311	GCATACTCATTAAGGaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	370
Sbjct	1386	dcatactcattaaggaaaaaaadtaccattgtgctaaacgctactgagactaaccaggaa	1445
Query	371	ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	430
Sbjct	1446	ACCCTAACGATGAAGATGGTCCTGTCCCGGGAGCGGCTGGCT	1505
Query	431	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	490
Sbjct	1506	ĠŦŦĠĊĀĠĠĀĊŦŦĊĀŦŦĊĀĀĀŦĀĠĠĀĀŦĀŦĊĀĠŦĊĊĀĀĠĊĀĀĠ	1565
Query	491	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	550
Sbjct	1566	ŤĠĠĂŤĂĠĠĂŤŤŤĠĊŤŤĂĂŤĠĠĊŤĠĂŤĠŤĂĂŤĂĂĠĂŤŤĠŤĂĊŤŤĊĊŤĂŤĂĊĂĠĂĠĠĊĂĊĊŤ	1625
Query	551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATA	610
Sbjct	1626	ŤĂĊŤĊŤĊŤĠĠĠĠĊĂŤŤĂŤĊĂĠĂŤŤŤŤĂĂŤĂĂĂŤĠĂĂŤĂĂĂŤĂ	1685
Query	611	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	670
Sbjct	1686	ŤĠŤĊĂĠĊŤĊŤŤĊĊĂŤĂĂŤŤĊĂĠŤĊŤĂĠĂŤĂĠĠĂĠĂŤŤĂŤŤŤĂĂĊŤĠĂĠĂ—–ŤĊŤŤĠĠŤĠ	1743
Query	671	AGTGTCAttttttttttttttttttttttttttttttttt	730
Sbjct	1744	AGTGTCATTTTTTTTTTTTTTTTTCTTTTTTTTGGTTTTTCAAGACAGGGTTT	1794
Query	731	CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	790
Sbjct	1795	CŤCŤĠŤĠŦĠGCCŤĠĠĊŤĠŤĊĊŤĠĠĂĀĊŤĊŤĠŤĂĠĂĊŤĠĠĠCŤĠĠĊĊŤĊĠĂĀĊŤĊĀĠĀĠĀ	1854
Query	791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC	850
Sbjct	1855	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCACCAGCTTGAAGTGTGTC	1914
Query	851	ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	910
Sbjct	1915	ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	1974
Query	911	TTGTGGCACCCAGTGACATCttttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA	970
Sbjct	1975	TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA	2034
Query	971	GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029
Sbjct	2035	GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG	2094
Query	1030	AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA	1088
Sbjct	2095	AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTCTCTGCAAATGAACAAAACA	2154
Query	1089	AAAC 1092      	
Sbjct	2155	ÀÀÀC 2158	

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic Sequence ID: **JN961338.1** Length: 38137 Number of Matches: 2 Range 1: 26029 to 27041

Score		Expect	Identities	Gaps	Strand	Frame	_
1740 bit	s(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus		•
Query	71	GTGGTGCCA	TTGGAATGTCAGCATTG	CTTGAGTGTCATGC	TGAGGGATGGT	CCTGACAGT	130
Sbjct	26029	GTGGTGCCA	TTGGAATGTCAGCATTG	CTTGAGTGTCATGC	TGAGGGATGGT	CCTGACAGT	26088
Query	131	AAACAGCGG	GAAGACACCAGGAGCAT'	TGTAATCGCTTGGT	TAATTGTCCGA	CATTGGTCC	190
Sbjct	26089	AAACAGCGG	ĠĀĀĠĀĊĀĊĊĠĠĠĀĠĊĀŤ'	TGTAATCGCTTGGT	TAATTGTCCGA	ĊATTĠĠŦĊĊ	26148

Query	191	AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	250
Sbjct	26149	AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	26208
Query	251	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT	310
Sbjct	26209		26268
Query	311	GCATACTCATTAAGGaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	370
Sbjct	26269	GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	26328
Query	371	ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	430
Sbjct	26329	Accetaacgatgaagatgeteetgteetgdeeggageggetggeteeacegaagtgetgggga	26388
Query	431	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	490
Sbjct	26389	dttdcaddacttcattcaaataddaatatcadtcaadcaad	26448
Query	491	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	550
Sbjct	26449	† dgataggatttgcttaatggctgatgtaataagattgtacttcctatacagaggcacct	26508
Query	551	TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATA	610
Sbjct	26509	ŢŖĊŢĊŢĠĠĠĠĊŖŢŢŖŢĊŖĠŖŢŢŢŢŖŖŢŢŢŢŢŢŢŢŢŢŢŢŢ	26568
Query	611	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	670
Sbjct	26569	ŤĠŤĊĀĠĊŤĊŤŤĊĊĂŤÁÁŤŤĊĀĠŤĊŤĀĠĂŤĀĠĠĀĠĂŤŤĀŤŤŤĀĀĊŤĠĀĀĠĀ—–ŤĊŤŤĠĠŤĠ	26626
Query	671	AGTGTCAttttttttttttttttttttttttttttttttt	730
Sbjct	26627	ÁĠŦĠŦĊĂŦŦŦŦŦŦŦŦĊŦŦŦŢŦŦĊ~~~~~ŦŦŦŦŦŦĠĠŦŦŦŦĊĂĂĠĂĊĀĠĠĠŦŦŦ	26677
Query	731	CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	790
Sbjct	26678	ĊŤĊŤĠŤĠŤĂĠĊĊĊŤĠĠĊŤĠŤĊĊŤĠĠĂĂĊŤĊŤĠŤĂĠĂĊŤĠĠĠĊŤĠĠĊĊŤĊĠĂĂĊŤĊĀĠĀĠĀ	26737
Query	791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC	850
Sbjct	26738	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGAAGTGTGTC	26797
Query	851	ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	910
Sbjct	26798	ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	26857
Query	911	TTGTGGCACCCAGTGACATC+t+t+t+tAATCAAGTGGACACACTTTTGATGTATTTCTCA	970
Sbjct	26858	TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA	26917
Query	971	GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029
Sbjct	26918 1030	GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA	26977 1088
Query Sbjct	26978	AGGTACAC-TTTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTTCT	27037
•	1089	AAAC 1092	21031
Query	27038	AAAC 1092      AAAC 27041	
Sbjct	2/038	AAAC 2/041	

Range 2: 37078 to 37200

Score		Exped	ct Identities	Gaps	Strand	Frame	1
141 bits	(76)	7e-29	() 108/123(88%)	4/123(3%)	Plus/Plus		
Query	682	ttttt	ctttcttttttttt	tttttttggttttttAA	GACAGGGTTT	CTCTGTGTAGC	741
Sbjct	37078	TTTTT	GTTTTTTGTTTTTTGT'	$egin{array}{c cccc} egin{array}{c ccccc} egin{array}{c ccccc} egin{array}{c cccc} egin{array}{c ccccc} egin{array}{c cccc} egin{array}{c cccc} egin{array}{c cccccc} egin{array}{c ccccccc} egin{array}{c ccccccc} egin{array}{c ccccc} egin{array}{c ccccc} egin{array}{c cccccc} egin{array}{c ccccc} egin{array}{c cccc} egin{array}{c ccccccc} egin{array}{c ccccccc} egin{array}{c cccccccc} egin{array}{c ccccccc} egin{array}{c cccccccc} egin{array}{c ccccc} egin{array}{c ccccc} egin{array}{c cccccc} egin{array}{c ccccccccc} egin{array}{c ccccccccccccccccccccccccccccccccccc$	GACAGGGTTT(	CTCTGTGTAGC	37137
Query	742	CCTGG	CTGTCCTGGAACTCT	GTAGACTGGGCTGGC	CTCGAACTCAC	GAGATCTGCCT	797
Sbjct	37138	CCTGG	CTGTCCTGGAGCTCACT	TTGTAGATCAGGCTGGC	CTCGAACTCAC	GAAATCTGCCT	37197
Query	798	GCC	800				
Sbjct	37198	GCC	37200				

Sequence ID: **JN951773.1** Length: 38097 Number of Matches: 2 Range 1: 25989 to 27001

1740 bits(942)       0.0()       999/1024(98%)       13/1024(1%)       Plus/Plus         Query       71       GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT         Sbjct       25989       GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT         Query       131       AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC         Sbjct       26049       AAACAGCGGGAAGACACCGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC         Query       191       AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT         Sbjct       26109       AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAACCATCTTT         Query       251       AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT         Sbjct       26169       AAATACGATAGAAAATAAGCTACTCAAGAACTGGTCTGTGTCCTTTTGCCTTAGTCCAT         Query       311       GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA         Sbjct       26229       GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA         Sbjct       26289       ACCCTAACGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	
Sbjct 25989 GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT  Query 131 AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC  Sbjct 26049 AAACAGCGGGAAGACACCGGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC  Query 191 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT  Sbjct 26109 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT  Query 251 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCCGTGTCCTTTTGCCTTAGTCCAT  Sbjct 26169 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT  Query 311 GCATACTCATTAAGGAAAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA  Sbjct 26229 GCATACTCATTAAGGAAAAAAAAGTACCATTGTGCTAAAACGCTACTGAGACTAACCAGGAA  Query 371 ACCCTAAAGGAAAAAAAAAGTACCATTGTGCTAAAACGCTACTGAGACTAACCAGGAA  Sbjct 26289 ACCCTAACGATGAAGATGTTCCTGTCCCGGGAGCGGCTGGCT	
Query       131       AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC         Sbjct       26049       AAACAGCGGGAAGACACCGGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC         Query       191       AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT         Sbjct       26109       AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT         Query       251       AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT         Sbjct       26169       AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT         Query       311       GCATACTCATTAAGGAAAAATAAGCTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA         Sbjct       26229       GCATACTCATTAAGGAAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA         Sbjct       26229       ACCCTAAAGATGAAGATGTCCTGTCCCCGGAGCGGCTGGCT	130
Sbjet 26049 AAACAGCGGGAAGACACCGGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC  Query 191 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT  Sbjet 26109 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT  Query 251 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT  Sbjet 26169 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT  Query 311 GCATACTCATTAAGGAAAAATAAGCTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA  Sbjet 26229 GCATACTCATTAAGGAAAAAAAAGTACCATTGTGCTAAAACGCTACTGAGACTAACCAGGAA  Query 371 ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	2604
Query 191 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT Sbjct 26109 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT Query 251 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT Sbjct 26169 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT Query 311 GCATACTCATTAAGGAAAAATAAGCTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA Sbjct 26229 GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA Query 371 ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	190
Sbjet 26109 AGGAACACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT  Query 251 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCCTTTTGCCTTAGTCCAT Sbjet 26169 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT Query 311 GCATACTCATTAAGGAAAAATAAGCTACCATGTGCTAAACGCTACTGAGACTAACCAGGAA Sbjet 26229 GCATACTCATTAAGGAAAAAAAAGTACCATTGTGCTAAAACGCTACTGAGACTAACCAGGAA Query 371 ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	2610
Query 251 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT Sbjct 26169 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT Query 311 GCATACTCATTAAGGAaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA Sbjct 26229 GCATACTCATTAAGGAAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA Query 371 ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	250
Sbjet 26169 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT  Query 311 GCATACTCATTAAGGaaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA  Sbjet 26229 GCATACTCATTAAGGAAAAAAAAGTTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA  Query 371 ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGCTCCACCGCAGTGCTGGGGA  Sbjet 26289 ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	2616
Query       311       GCATACTCATTAAGGaaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA         Sbjct       26229       GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA         Query       371       ACCCTAAAGATGAAGATGTCCTGTCCCCGGAGCGGCTGGCT	310
Sbjet 26229 GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA  Query 371 ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGCTCCACCGCAGTGCTGGGGA Sbjet 26289 ACCCTAACGATGAAGATGTCCTGTCCCGGGAGCGGCTGCTCCACCGCAGTGCTGGGGA  Query 431 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGCCAG Sbjet 26349 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGCTGATACGTGAGTGGCAG  Query 491 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT Sbjet 26409 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	2622
Query       371       ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	370
Sbjet 26289 ACCCTAACGATGAAGATGGCCTGTCCCGGGAGCGGCTGCTCCACCGAAGTGCTGGGGA  Query 431 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG Sbjet 26349 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGCTGATACGTGAGTGGCAG  Query 491 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT Sbjet 26409 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	2628
Query       431       GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG         Sbjct       26349       GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAG	430 2634
Sbjct 26349 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAG	490
Query 491 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT Sbjct 26409 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	2640
Sbjet 26409 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	550
	2646
-	610
Sbjct 26469 TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATGGTATTTTTTTAAA	2652
Query 611 TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	670
Sbjct 26529 TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA—TCTTGGTG	2658
Query 671 AGTGTCAttttttttttttttttttttttttttttttttt	730
Sbjct 26587 AGTGTCATTTTTTTTTTTTTTTCTTTTTTTGGTTTTTCAAGACAGGGTTT	2663
Query 731 CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGCCTGGCCTCGAACTCAGAGA	790
sbjet 26638 chchdreitedechdechdechdechdechdechdechdechdechdec	2669
Query 791 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCAGCTTGATGTGTCTC	850
sbjet 26698 tétécéttécéttéctédédátékédédététédédédédédédédtététété	2675
Query 851 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	910
Sbjet 26758 ÁŤŤŤÁÁÁÁČĊÁĊŤĠŤŤŤÁÁŤÁÁČĊČŤÁČÁĠÁČÁŤĠÁÁŤĊŤĠĠÁŤÁÁŤĠČŤÁĠĠŤÁŤÁÁÁČ	2681
Query 911 TTGTGGCACCCAGTGACATCttttttttAATCAAGTGGACACCTTTTGATGTATTTCTCA	970
Sbjet 26818 ŤŤĠŤĠĠĊĂĊĊĂĠŤĠĂĊĂŤĊŤŤŤŤŤŤŤĂŤĊĂĂĠŤĠĠĂĊĂĊĂĊŤŤŤŤĠĂŤĠŤĂŤŤŤĊŤĊĂ	2687
Query 971 GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029
Sbjct 26878 ĠŤŤÁĊÁÁÁĠĊŤĠÁĊŤŤŤŤŤŤŤŤÁÁŤĠÁÁĠĠĠÁÁŤÁÁŤŤĠĊĊÁÁĠŤÁĊŤŤÁÁÁŤĊŤÁĊĊŤG  Query 1030 AGGTACAC-TTTAGACCTCATCTTCTATTTCTCCCTCTCTCTTCTGCAAATGAACAAAACA	2693 1088
Query 1030 AGGTACAC-TTTAGACCTCATCTTCTATTTCTCCCTCTCTTCTGCAAATGAACAAAACA	2699
Query 1089 AAAC 1092	2033
Sbjct 26998 AAAC 27001	

Range 2: 37038 to 37160

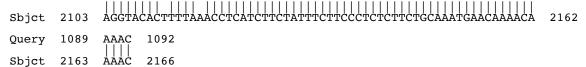
Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	7e-29()	108/123(88%)	4/123(3%)	Plus/Plus	

Query	682	ttttctttcttttttttttttttttggttttttAAGACAGGGTTTCTCTGTGTAGC	741
Sbjct	37038	TTTTTGTTTTTTGTTTTTGTTTTTGTTTTTTTTAAGACAGGGTTTCTCTGTGTAGC	37097
Query	742	CCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGATCTGCCT	797
Sbjct	37098	CCTGGCTGTCCTGGAGCTCACTTTGTAGATCAGGCTGGCCTCGAACTCAGAAATCTGCCT	37157
Query	798	GCC 800	
Sbjct	37158	GCC 37160	

Mus musculus sterol-C5-desaturase (Sc5d), mRNA

Sequence ID: **NM\_172769.2** Length: 2249 Number of Matches: 1 Range 1: 1154 to 2166

Sbjet 1154 GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCAGGGATGGTCCTGACAGT 12 Query 131 AAACAGCGGGAAGACACCAGGAGCATTGTTAATCGCTTGGTTAATTGTCCGACATTGGTC 19 Sbjet 1214 AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTC 19 Sbjet 1274 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGAAGCATCTTAACAGAGCATCTT 25 Sbjet 1274 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGAAGCATCTTGAGCCATCTT 13 Query 251 AAATACGATACAAAAATAACTTACTCAAGAAGCTGGTCTGTGTCCTTTGCCTTAGTCCAT 13 Sbjet 1334 AAATACGATACAAAAATAACTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT 13 Sbjet 1394 GCATACTCATTAAGGAAAAAAAAAAACTACCATTGTGCTAAACGCTACTGAGCATCAACCAGGAA 14 Query 371 ACCCTAAAGATGAAGAATGTCCATTGTGCTAAACGCTACTGAGCATCAACCAGGAA 14 Sbjet 1454 ACCCTAACGATGAAGATGTCCTCTCCCGGAGCGGCTGCTCCACCCAC	Score		Expect	Identities	Gaps	Strand	Frame	
SBjet 1154 GTGGTGCATTGGAATGTCAGCATTGCTTGAGTGTCAGGGATGGTCCTGACAGT 12 Query 131 AAACAGCGGGAAGACACCAGGAGCATTGTTAATCGCTTGGTTAATTGTCCGACATTGGTC 19 Sbjet 1214 AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTC 19 Sbjet 1274 AGGAACACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGAAGCTCTGAAGCATCTT 25 Sbjet 1274 AGGAACACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGAAGCTCTGAAGCATCTT 13 Query 251 AAATACGATACAAAAATAACTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT 13 Sbjet 1334 AAATACGATACAAAAATAACTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT 13 Sbjet 1394 GCATACTCATTAAGGAAAAAATAACCTCTCAAGAAGCTGCTCATAACGCTACTGAGCATCAACCAGGAA 14 Query 371 ACCCTAAAGATGAAGATGTCCTTCTGCCCGGAGCCGTCTCACCCCAGTGCTGAGCATAACCAGGAA 14 Sbjet 1454 ACCCTAAAGATGAAGATGTCCTTCCCCGGAGCGGCTGCTCCACCGCAGTGCTGGGGA 15 Sbjet 1514 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAG	1740 bit	s(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus		
Query 131 AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC 19 Sbjet 1214 AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTC 12 Query 191 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT 25 Sbjet 1274 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT 13 Query 251 AAATACGATAGAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT 13 Sbjet 1334 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT 13 Query 311 GCATACTCATTAAGGAAAATAAGCTACCATTGGTCTAAACCATCACCAGGAA 37 Sbjet 1394 GCATACTCATTAAGGAAAATAAGCTACCATTGGTCTAAACCATCACCAGGAA 14 Query 371 ACCCTAAAGATGAAAATAAGCTACCATTCCCGGAGCGGTGGCTCCACCGCAGTGCTGGGA 13 Sbjet 1454 ACCCTAACGATGAAAATAAGGTTCCTTCCCGGGAGCGGTGGCTCCACCGCAGTGCTGGGA 15 Sbjet 1514 GTTGCAGGACTTCATTCAAATAGGAAATACAGTCCAAGCACTAACCAGGAA 15 Sbjet 1514 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCACTAACCAGGAG 15 Query 491 TGGATAGGATTTGCTTAATGGCTGATGTAACTCAAGCAGCTGATACCTGAGGCACCC 55 Sbjet 1574 TACTCTCTGGGGCATTATCAAATTAGAATTAAAATAAAA	Query	71	GTGGTGCCAT	TGGAATGTCAGCAT	TGCTTGAGTGTCATGC	TGAGGGATGGTC	CTGACAGT	13
Sbjet 1214 AAACAGGGGAAGACCGGGAGCATTGTTAATTGTTCGTTAATTGTCCGACATTGGTCC 12 Query 191 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCACTTGTT 25 Sbjet 1274 AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT 13 Query 251 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCCTTAGTCCAT 13 Sbjet 1334 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTTCCCTTAGTCCAT 13 Query 311 GCATACTCATTAAGGAAGAAGAAGCTGTTCATGTGCTAAACGCTACTGAGACTAACCAGGAA 37 Sbjet 1394 GCATACTCATTAAGGAAAAAAACTTCCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 14 Query 371 ACCCTAAAGATGAAGATGTTCCTTGTCCCGGGAGCGGCTGGCT	Sbjct	1154	GTGGTGCCAT	rggaatgtcagcai	TGCTTGAGTGTCATGC	TGAGGGATGGTC	CTGACAGT	12
Query         191         AGGAACAACTTGTCTTTTCAGCCGGCTGAGCCTGCAGCCTGTACAGCTCTGAAGCATCTTT         25           Sbjet         1274         AGGAACAACTTGTCTTTTCAGCCGGCTGAGCCTGCAGCCTGTACAGCTCTGAAGCATCTTT         13           Query         251         AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT         31           Sbjet         1334         AAATACCATAGAAAATAAGCTACTAAGAAGCTGGCTAAACGCTACTGAGACTAACCAGGAA         37           Sbjet         1394         GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA         14           Query         371         ACCCTAAACGATGAAGATGTTCCTGTCCCCGGGAGCGGCTGGCT	Query	131	AAACAGCGGG.	AAGACACCAGGAGC	CATTGTAATCGCTTGGT	TAATTGTCCGAC	ATTGGTCC	19
Sbjet 1274 AGGAACACTTGTCTTTTCACCCGGCTGACCTGCAGCTGTACAGCTCTGAAGCACTTTT 13 Query 251 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTGTCCTTTTTGCCTTAGTCCAT 31 Sbjet 1334 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTTGCCTTAGTCCAT 31 Query 311 GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 37 Sbjet 1394 GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 14 Query 371 ACCCTAAAGATGAAGATGTTCCTGTCCCCGGGAGCGGCTGGCT	Sbjct	1214	AAACAGCGGG.		cktrigtkktcigctriggt	TAATTGTCCGAC	ATTGGTCC	12
Query         251         AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGCCTTTTGCCTTAGTCCAT         31           Sbjet         1334         AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGCCTTTTGCCTTAGTCCAT         13           Query         311         GCATACTCATTAAGGAAAAATAAGCTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA         37           Sbjet         1394         GCATACTCATTAAGGAAAAATAAGCTACTTCCTCGCGGAGCGGCTGCTCCACCGCAGTGCTGGGGA         43           Query         371         ACCCTAAACATGAAGATGTTCCTGTCCCGGGAGCGGCTGGCT	_		AGGAACAACT	IGTCTTTTCAGCCG 	GCTGACCTGCAGCCTG	TACAGCTCTGAA	GCATCTTT	25
Sbjet 1334 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGCCTTTTGCCTTAGTCCAT 13 Query 311 GCATACTCATTAAGGABABAGAGAGCTGGTCTGTGCCTTTTGCCTTAGTCCAT 37 Sbjet 1394 GCATACTCATTAAGGABABAGAGACAAAGCTAACCAGGAA 37 Sbjet 1394 GCATACTCATTAAGGABABAGAGACACATTGTGCTAAAACGCTACTGAGACTAACCAGGAA 14 Query 371 ACCCTAAAGATGAAGATGTTCCTGTCCCGGAGCGGCTGCCTCCACCGAAGTGCTGGGGA 43 Sbjet 1454 ACCCTAACGATGAAGATGTTCCTGTCCCGGGAGCGGCTGGCT	•							13
Query         311         GCATACTCATTAAGGABABABABATACCATTGTGCTAAACCGCTAACTGAGACTAACCAGGAA         37           Sbjct         1394         GCATACTCATTAAGGABABABATGTCCTGTCTGAGACTTAACCAGGAA         14           Query         371         ACCCTAAAGATGABAGATGTTCCTGTCCCCGGAGCGGCTGGCTCCACCGAGTGCTGGGGA         43           Sbjct         1454         ACCCTAAAGATGABAGATGGTCCTGTCCCCGGAGCGGCTGGCTCCACCGAAGTGCTGGGGA         15           Query         431         GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG         49           Sbjct         1514         GTTGCAGGACTTCATTCAAATAGGATTATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG         15           Query         491         TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT         55           Sbjct         1574         TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT         16           Query         551         TACTCTCTGGGGCATTATCAGATTTTAATAAATAAATAAA	_							31
Sbjet 1394 GCATACTCATTAAGGAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 14 Query 371 ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT								
Query371ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCT	_							
Sbjet 1454 ACCCTAACGATGATCATTCAAATAGGAATATCAGTCCAAGCAGGCTGGCT								
Query 431 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG 49 Sbjct 1514 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAG	_							
Sbjet 1514 GTTGCAGGACTTCATTCAAATAGGAATATCAGCCAGCAGCTGATACGTAGACGCAGC Query 491 TGGATAGGATTTGCTTAATGGCTGATACAGAAGAGCACCT 55 Sbjet 1574 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT 16 Query 551 TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATA	•							
Query491TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT55Sbjet1574TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT16Query551TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATA	_					AGCTGATACGTG	AGTGGCAG	
Query 551 TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATA	-	491	ŢĢĢĄŢĄĢĢĄŢ	ГТĢСТТААТĢĢСТĢ	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	СТТССТАТАСАG	ĄĢĢÇĄÇÇŢ	55
Sbjet 1634 TACTCTCTGGGCATTATCAGATTTTAATAAATGAATAAATGATATTTTTTTAAA 16 Query 611 TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG 67 Sbjet 1694 TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA——TCTTGGTG 17 Query 671 AGTGTCACTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA——TCTTGGTG 17 Sbjet 1752 AGTGTCATTTTTTTTTCTTT—TTTC————TTTTTTTGGTTTTTCAAGACAGGGTTT 18 Query 731 CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 79 Sbjet 1803 CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 18 Query 791 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCACCTGCCCAGCTTGATGTGTC 85 Sbjet 1863 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCTGCCCAGCTTGAAGTGTGTC 19 Sbjet 1923 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 19 Query 911 TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTTGATGTATTTCTCA 97 Sbjet 1983 TTGTGGCACCCAGTGACATCTTTTTTTTTAATCAAGTGGACACACTTTTTTTT	Sbjct	1574	 TGGATAGGAT	  TGCTTAATGGCTG		 CTTCCTATACAG	 GAGGCACCT	16
Query 611 TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG 67 Sbjet 1694 TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGAGTTATTTAACTGAAGA—TCTTGGTG 17 Query 671 AGTGTCAttttttttttttttttttttttttttttttttt	Query	551	TACTCTCTGG	GGCATTATCAGATT	TTAATAAATGAATAAA	TAAATGGTAttt	tttttAAA	61
Sbjct 1694 TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA—TCTTGGTG 17  Query 671 AGTGTCAttttttttttttttttttttttttttttttttt	Sbjct	1634	TACTCTCTGG			 TAAATGGTATTT	 TTTTTTAAA	16
Query 671 AGTGTCAttttttttttttttttttttttttttttttttt	Query	611	TGTCAGCTCT	TCCATAATTCAGTC	TAGATAGGAGATTATT	TAACTGAAGATC	TCTTGGTG	67
Sbjet 1752 AGTGTCATTTTTTTTTTTTTTCTTT—TTTC———TTTTTTTGGTTTTTCAAGACAGGGTTT 18  Query 731 CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 79  Sbjet 1803 CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 18  Query 791 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCACCTGCCCAGCTTGATGTGTGTC 85  Sbjet 1863 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCACCTGCCCAGCTTGAAGTGTGTC 19  Query 851 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 91  Sbjet 1923 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 19  Query 911 TTGTGGCACCCAGTGACATCttttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA 97  Sbjet 1983 TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTTGATGTATTTCTCA 20  Query 971 GTTACAAAGCTGAC—tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 10  Sbjet 2043 GTTACAAAGCTGAC—tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 21	Sbjct	1694	TGTCAGCTCT	rccataattcagtc	TAGATAGGAGATTATT	TAACTGAAGA	TCTTGGTG	17
Query 731 CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 79 Sbjct 1803 CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA 18 Query 791 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC 85 Sbjct 1863 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGAAGTGTGTC 19 Query 851 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 91 Sbjct 1923 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 19 Query 911 TTGTGGCACCCAGTGACATCtttttttaATCAAGTGGACACACTTTTTGATGTTTTTCTCA 97 Sbjct 1983 TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTTGATGTATTTCTCA 20 Query 971 GTTACAAAGCTGAC-tttttttaATCAAGTGGACACACTTTTTGATGTATTTCTCA 20 Sbjct 2043 GTTACAAAGCTGAC-ttttttttaATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 21 Sbjct 2043 GTTACAAAGCTGACTTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 21	Query	671	AGTGTCAttt	ttttttctttcttt	tttttttttttttt	ggttttttAAGA	CAGGGTTT	73
Sbjet 1803 CTCTGTGTAGCCCTGGCTGTCCTGGAACTCGTAGACTGGGCTGGCCTCGAACTCAGAGA 18  Query 791 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCACCCAGCTTGATGTGTGTC 85  Sbjet 1863 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCACCTGCCCAGCTTGAAGTGTGTC 19  Query 851 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 91  Sbjet 1923 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 19  Query 911 TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA 97  Sbjet 1983 TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTTGATGTATTTCTCA 20  Query 971 GTTACAAAGCTGAC-tttttttAATCAAGTGGACACACTTTTTAATCACCTA 10  Sbjet 2043 GTTACAAAGCTGAC-TTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 21	Sbjct	1752	AĠŦĠŦĊĀŦŦŦ	<u> </u> ተተተተተተረተተተ ተተ	rc	GGTTTTTCAAGA	ckśśśttt	18
Query 911 TTGTGGCACCCAGTGACATCACAGACATGACTGCCCAGCTTGATGTGTCC 97 Sbjct 1983 TTGTGGCACCCAGTGACATCACAGACATGAATCTGATGATATACAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 91 Sbjct 1923 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 91 Sbjct 1923 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 92 Query 911 TTGTGGCACCCAGTGACATCTTTTAATAACCCTACAGACATGAATCTTGATGTATTTCTCA 97 Sbjct 1983 TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA 20 Query 971 GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 10 Sbjct 2043 GTTACAAAGCTGACTTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 21	Query		CTCTGTGTAG	CCCTGGCTGTCCTG 	GAACTCTGTAGACTGG	GCTGGCCTCGAA	CTCAGAGA	79
Sbjct 1863 TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCACCTGCCCAGCTTGAAGTGTGTC 19  Query 851 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 91  Sbjct 1923 ATTTAAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 19  Query 911 TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA 97  Sbjct 1983 TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA 20  Query 971 GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 10  Sbjct 2043 GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 21	Sbjct							18
Query 911 TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA 97 Sbjct 1983 TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA 20 Query 971 GTTACAAAGCTGAC-ttttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA 20 Sbjct 2043 GTTACAAAGCTGAC-ttttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 21								
Sbjct 1923 ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC 19  Query 911 TTGTGGCACCCAGTGACATCttttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA 97  Sbjct 1983 TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA 20  Query 971 GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 10  Sbjct 2043 GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 21	_							
Query     911     TTGTGGCACCCAGTGACATCTTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA     97       Sbjct     1983     TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA     20       Query     971     GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA     10       Sbjct     2043     GTTACAAAGCTGACTTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG     21								
Sbjct 1983 TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGATGTATTTCTCA 20  Query 971 GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 10  Sbjct 2043 GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 21	_							
Query 971 GTTACAAAGCTGAC-tttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA 10 Sbjct 2043 GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 21								
Sbjct 2043 GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG 21	_							10
								21
	_		AGGTACAC-T	TTAGACCTCATCTT	CTATTTCTTCCCTCTC	TTCTGCAAATGA	ACAAAACA	10



Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence Sequence ID: AC160051.2 Length: 199433 Number of Matches: 3

Range 1: 34694 to 35706

Score		Expect	Identities	Gaps	Strand	Frame
1740 bits	s(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus	
Query	71	GTGGTGCCA	TTGGAATGTCAGCA	ATTGCTTGAGTGTCATGC	TGAGGGATGGT	CCTGACAGT
Sbjct	34694	GTGGTGCCA	ttggaatgtcagc	AttGcttGAGtGtcAtGc	trgagggatggt	CCTGACAGT
Query	131	AAACAGCGG	GAAGACACCAGGA(	GCATTGTAATCGCTTGGT 	TAATTGTCCGA	CATTGGTCC
Sbjct	34754			ĠĊĂŢŢĠŢĂĂŢĊĠĊŢŢĠĠŢ		
Query	191			CGGCTGACCTGCAGCCTG		
Sbjct	34814			CGGCTGACCTGCAGCCTG		
Query Sbjct	251 34874			CTCAAGAAGCTGGTCTGT 		
Query	311			STACCATTGTGCTAAACG		
Sbjct	34934					
Query	371			ГĢТÇÇÇÇĞĞAĞÇĞĞÇТĞĞ		
Sbjct	34994	 ACCCTAACG		  GTCCCGGGAGCGGCTGG	 CTCCACCGAAG	 TGCTGGGGA
Query	431	GTTGCAGGA	CTTCATTCAAATAG	GGAATATCAGTCCAAGCA	GGCTGATACGT	GAGTGGCAG
Sbjct	35054	GTTGCAGGA	CTTCATTCAAATAG		AGCTGATACGT	GAGTGGCAG
Query	491	TGGATAGGA	TTTGCTTAATGGC	rgatgtaataagattgta 	CTTCCTATACA	GAGGCACCT
Sbjct	35114	TĠĠÀTÀĠĠÀ	tttgcttaatgcc:	rgatgtaataagattgta	cttcctataca	ĠĀĠĠĊĀĊĊŦ
Query	551	TACTCTCTG	GGGCATTATCAGA:		TAAATGGTAtt	ttttttAAA 
Sbjct	35174			rtraataatgaataa		
Query	611			CTAGATAGGAGATTATT 		
Sbjct Query	35234 671			rCTAGATAGGAGATTATT cttttttttttttttttt		
Sbjct	35292					
Query	731			rggaactctgtagactgg		
Sbjct	35343	 CTCTGTGTA			 GCTGGCCTCGA	 ACTCAGAGA
Query	791	ТСТСССТСС	CCTTGCTGGGATC	AGAGGTGTGCACCACCAC	TGCCCAGCTTG	ATGTGTGTC
Sbjct	35403	TCTGCCTGC				 AAGTGTGTC
Query	851	ATTTAAAAC	CACTGTTTAATAA(	CCCTACAGACATGAATCI	GGATAATGCTA	GGTATAAAC
Sbjct	35463	ATTTAAAAC	CACTGTTTAATAA	CCTACAGACATGAATCT	'ddataatgcta	GGTATAAAC
Query	911	TTGTGGCAC	CCAGTGACATCttt	ttttaatcaagtggaca	CACTTTTGATG	TATTTCTCA
Sbjct	35523			ŗŢŢŢŢŖŖŢĊŖŖĠŢĠĠŖĊŖ	ĊĂĊŤŤŤŤĠĂŤĠ	
Query	971					
Sbjct	35583			ÄÄTĠÄÄĠĠĠÄÄTÄÄŤTĠĊ		
Query	1030			FTCTATTTCTTCCCTCTC		
Sbjct Query	35643 1089	AAAC 109		FTCTATTTCTTCCCTCTC	.1 TCTGCAAATG	AACAAAACA
Suer A	1009		۷.			

Sbjct 35703 AAAC 35706

Range 2: 45743 to 45865

Score		Expect	Identities	Gaps	Strand	Frame	i
141 bits	(76)	7e-29()	108/123(88%)	4/123(3%)	Plus/Plus		
Query	682	tttttct	ttctttttttttt	ttttttggttttttAA	GACAGGGTTT(	CTCTGTGTAGC	741
Sbjct	45743	TTTTTGT	TTTTTGTTTTTTTGTT'	$egin{array}{cccccccccccccccccccccccccccccccccccc$	GACAGGGTTT(	CTCTGTGTAGC	45802
Query	742	CCTGGCT	GTCCTGGAACTCT-	-GTAGACTGGGCTGGC	CTCGAACTCAG	GAGATCTGCCT	797
Sbjct	45803	CCTGGCT	GTCCTGGAGCTCACTT	TGTAGATCAGGCTGGC	CTCGAACTCA	GAAATCTGCCT	45862
Query	798	GCC 80	0				
Sbjct	45863	GCC 45	865				

Range 3: 139035 to 139134

Score		Expect	Identities	Gaps	Strand	Frame	
110 bits	(59)	2e-19()	87/100(87%)	4/100(4%)	Plus/Minus		
Query	705	ttttttc	gttttttAAGACAG	GGTTTCTCTGTGTA	GCCCTGGCTGTC	CTGGAACTC	760
Sbjct	139134	TTTGTT	GCTTTTTGAGACAG	GGTTTCTCTGTGTA	GCCCTGGCTGTC	CTGGAACTCACTC	139075
Query	761	TGTAGAC	TGGGCTGGCCTCGA.	ACTCAGAGATCTGC	CTGCC 800		
Sbjct	139074	TGTAGAC	CAGGCTGGCCTTGA	ACTCAGAAATCCAC	CTGCC 13903	5	

Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence

Sequence ID: AK077670.1 Length: 2207 Number of Matches: 1

Range 1: 1112 to 2124

Score		Expect	Identities	Gaps	Strand	Frame	_
1740 bit	s(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus		
Query	71	GTGGTGCCATT	rggaatgtcagcattgc	TTGAGTGTCATGCT	GAGGGATGGTC	CTGACAGT	130
Sbjct	1112	GTGGTGCCAT	rggaatgtcagcattgc	TTGAGTGTCATGCT	 GAGGGATGGTC	CTGACAGT	1171
Query	131	AAACAGCGGGA	AAGACACCAGGAGCATT	GTAATCGCTTGGTT	AATTGTCCGAC	ATTGGTCC	190
Sbjct	1172	AAACAGCGGG	AAGACACCGGGAGCATT		AATTGTCCGAC	ATTGGTCC	1231
Query	191	AGGAACAACT	rgtcttttcagccggct	GACCTGCAGCCTGT	ACAGCTCTGAA	GCATCTTT	250
Sbjct	1232	AGGAACAACT	rgrctrtrcagccggcr	GACCTGCAGCCTGT	ACAGCTCTGAA	GCATCTTT	1291
Query	251	AAATACGATAO	GAAAATAAGTTACTCAA	GAAGCTGGTCTGTG	TCCTTTTGCCT	TAGTCCAT	310
Sbjct	1292	AAATACGATA	GAAAATAAGCTACTCAA	GAAGCTGGTCTGTG	TCCTTTTGCCT	TAGTCCAT	1351
Query	311	GCATACTCAT	TAAGGaaaaaaaGTACC	ATTGTGCTAAACGC	TACTGAGACTA	ACCAGGAA	370
Sbjct	1352	GCATACTCAT	TAAGGAAAAAAAGTACC.	ATTGTGCTAAACGC	TACTGAGACTA	ACCAGGAA	1411
Query	371	ACCCTAAAGAT	rgaagatgttcctgtcc	CCGGAGCGGCTGGC	TCCACCGCAGT	GCTGGGGA	430
Sbjct	1412	ACCCTAACGA	rgaagatggtcctgtcc	CGGGAGCGGCTGGC	TCCACCGAAGT	GCTGGGGA	1471
Query	431	GTTGCAGGACT	TTCATTCAAATAGGAAT	ATCAGTCCAAGCAG	GCTGATACGTG	AGTGGCAG	490
Sbjct	1472	GTTGCAGGAC	TTCATTCAAATAGGAAT.	ATCAGTCCAAGCAA	GCTGATACGTG	AGTGGCAG	1531
Query	491	TGGATAGGAT	TTGCTTAATGGCTGATG	TAATAAGATTGTAC	TTCCTATACAG	AGGCACCT	550
Sbjct	1532	TGGATAGGAT	TTGCTTAATGGCTGATG	TAATAAGATTGTAC	TTCCTATACAG	AGGCACCT	1591
Query	551	TACTCTCTGG	GCATTATCAGATTTTA	ATAAATGAATAAAT	AAATGGTAttt	tttttAAA	610
Sbjct	1592	TACTCTCTGG				 TTTTTAAA	1651

Query	611	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	670
Sbjct	1652	tgtcagctcttccataattcagtctagataggagattatttaactgaagatcttggtg	1709
Query	671	AGTGTCAttttttttttttttttttttttttttttttttt	730
Sbjct	1710	AGTGTCATTTTTTTTTTTTTTTCTTTTTTTTGGTTTTTTCAAGACAGGGTTT	1760
Query	731	CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	790
Sbjct	1761	ctctgtgtagccctggctgtcctggaactctgtagactgggctggcctcgaactcagaga	1820
Query	791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCTGCCCAGCTTGATGTGTC	850
Sbjct	1821	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGAAGTGTGTC	1880
Query	851	ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	910
Sbjct	1881	ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	1940
Query	911	TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA	970
Sbjct	1941	TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA	2000
Query	971	GTTACAAAGCTGAC-ttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029
Sbjct	2001	GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG	2060
Query	1030	AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA	1088
Sbjct	2061	AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTTCT	2120
Query	1089	AAAC 1092	
Sbjct	2121	AAAC 2124	

Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence

Sequence ID: AK043825.1 Length: 2209 Number of Matches: 1

Range 1: 1113 to 2125

Score		Expect	Identities	Gaps	Strand	Frame	
1740 bit	s(942)	0.0()	999/1024(98%)	13/1024(1%)	Plus/Plus		_
Query	71	GTGGTGCCAT'	rggaatgtcagcat	TGCTTGAGTGTCATGC	CTGAGGGATGGTC	CTGACAGT	130
Sbjct	1113	GTGGTGCCAT		TGCTTGAGTGTCATGC	CTGAGGGATGGTC	CTGACAGT	1172
Query	131	AAACAGCGGG	AAGACACCAGGAGC	ATTGTAATCGCTTGGT	TTAATTGTCCGAC	ATTGGTCC	190
Sbjct	1173	AAACAGCGGG	AAGACACCGGGAGC	ATTGTAATCGCTTGG	TTAATTGTCCGAC	ATTGGTCC	1232
Query	191	AGGAACAACT	rgtcttttcagccg	GCTGACCTGCAGCCTC	GTACAGCTCTGAA	GCATCTTT	250
Sbjct	1233	AGGAACAACT	rGTCTTTTCAGCCG	GCTGACCTGCAGCCT	GTACAGCTCTGAA	GCATCTTT	1292
Query	251	AAATACGATA	GAAAATAAGTTACT	CAAGAAGCTGGTCTG	rgtccttttgcct	TAGTCCAT	310
Sbjct	1293	AAATACGATA	GAAAATAAGCTACT	chadaadctddtctd	tgtccttttgcct	TAGTCCAT	1352
Query	311	GCATACTCAT	raaggaaaaaaagt 	ACCATTGTGCTAAAC	GCTACTGAGACTA	ACCAGGAA	370
Sbjct	1353	GCATACTCAT'	raaggaaaaaaadt	ACCATTGTGCTAAACC	GCTACTGAGACTA	ACCAGGAA	1412
Query	371	ACCCTAAAGA	rgaagatgttcctc	TCCCCGGAGCGGCTGC	GCTCCACCGCAGT	GCTGGGGA	430
Sbjct	1413	ACCCTAACGA:	rgyygyr	stccceeepecece	gctccaccgaagt	ĠĊŦĠĠĠĠĀ	1472
Query	431	GTTGCAGGAC'	TTCATTCAAATAGG	GAATATCAGTCCAAGC	AGGCTGATACGTG	AGTGGCAG	490
Sbjct	1473	ĠTTĠĊAĠĠĀĊ	rtcattcaaatagd	saatatcagtccaagc <i>i</i>	AAGCTGATACGTG	ÅĠŦĠĠĊĀĠ	1532
Query	491	TGGATAGGAT	TTGCTTAATGGCTG	ATGTAATAAGATTGTA	ACTTCCTATACAG	AGGCACCT	550
Sbjct	1533	TGGATAGGAT!	rtgcttaatggctg	satgtaataagattgt	Acttcctatacad	AGGCACCT	1592
Query	551	TACTCTCTGG	GGCATTATCAGATT	TTAATAAATGAATAA 	ATAAATGGTAttt	tttttAAA	610
Sbjct	1593	TACTCTCTGG	ggcattatcagatt	rttaataaatgaataa	Ataaatggtatt	†††††AAA	1652
Query	611	TGTCAGCTCT	rccataattcagtc 	TAGATAGGAGATTATT	TTAACTGAAGATC	TCTTGGTG	670

Sbjct	1653	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTTGGTG	1710
Query	671	AGTGTCAttttttttttttttttttttttttttttttttt	730
Sbjct	1711	AGTGTCATTTTTTTTTTTTTTTTCTTTTTTTTGGTTTTTCAAGACAGGGTTT	1761
Query	731	CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	790
Sbjct	1762	CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	1821
Query	791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC	850
Sbjct	1822	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGAAGTGTGTC	1881
Query	851	ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	910
Sbjct	1882	Atttaaaaccactgtttaataaccctacagacatgaatctggataatgctaggtataaac	1941
Query	911	TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA	970
Sbjct	1942	TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA	2001
Query	971	GTTACAAAGCTGAC-ttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029
Sbjct	2002	GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG	2061
Query	1030	AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAACAAAACA	1088
Sbjct	2062	AGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCTCTCTGCAAATGAACAAAACA	2121
Query	1089	AAAC 1092	
Sbjct	2122	AAAC 2125	

PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA

Sequence ID: XM\_029481771.1 Length: 2336 Number of Matches: 1

Range 1: 1184 to 2198

Score		Expect	Identities	Gaps	Strand	Frame	
1576 bit	s(853)	0.0()	970/1025(95%)	13/1025(1%)	Plus/Plus		
Query	71	GTGGTGCCAT	TGGAATGTCAGCATT	GCTTGAGTGTCATGC	TGAGGGATGGTC	CTGACAGT	130
Sbjct	1184	GTGGTGCCAT	   TTGAATGTCAGCATT	GCTTGAGTGTCATGC	 TGAGGGATGGTC	CTGACAGT	1243
Query	131	AAACAGCGGG.	AAGACACCAGGAGCA	TTGTAATCGCTTGGT	TAATTGTCCGAC	ATTGGTCC	190
Sbjct	1244	AAACAGCGGG.	AAGGCACCGGGAGCA	ATTGTAATCTCTTGGT	TAATTGTCCGAC	ATTGGTCC	1303
Query	191	AGGAACAACT	TGTCTTTTCAGCCGG	CTGACCTGCAGCCTG	TACAGCTCTGAA	GCATCTTT	250
Sbjct	1304	AGGAACAATT	tgtcttttcagccg	ctdacctdcadcctd	TACAGCTCCGAA	GCATCTTT	1363
Query	251	AAATACGATA	GAAAATAAGTTACTC	CAAGAAGCTGGTCTGT	GTCCTTTTGCCT	TAGTCCAT	310
Sbjct	1364	AAATACGATA	daaaataadctactc	chagahactggtctgc	ĠŦĊĊŦŦŦŦĠĊĊĪ	TAATCCAT	1423
Query	311	GCATACTCAT	TAAGGaaaaaaaGTA 	CCATTGTGCTAAACG	CTACTGAGACTA	ACCAGGAA	370
Sbjct	1424	ĠĊĀŦĀĊŦĊĀŦ	TAAGGAAAAAAAGTA	\ccattgtgctragcg	ĊŦĀĊŦĠĀĠĀĊŦĀ	ACCAGGAA	1483
Query	371	ACCCTAAAGA	TGAAGATGTTCCTGT 	CCCCGGAGCGGCTGG	CTCCACCGCAGT	'GCTGGGGA	430
Sbjct	1484	ACCCTAAAGA	†ĠĀĀĠ†ĠC†ĊĊĊĠ†	ŢĊĊĊĠĠĀĠŦĠĠĊĊĠĠ	ĊŦĠĊĀĊĀĠĊĀĠŦ	ĠĊĠĠĠĀ	1543
Query	431	GTTGCAGGAC	TTCATTCAAATAGGA 	ATATCAGTCCAAGCA	GGCTGATACGTG	AGTGGCAG	490
Sbjct	1544	ĠĊŦĠĊĀĠĠĀĊ	ŤŤĊÁŤŤĊÁGÁŤÁĠĠÁ	AGTATCAGTCCAAGCA	ĠĠĊŦĠÀŦÀĊĠŦĠ	ÄĠŤĠĠĊĀĠ	1603
Query	491	TGGATAGGAT	TTGCTTAATGGCTGA 	TGTAATAAGATTGTA	CTTCCTATACAG	AGGCACCT	550
Sbjct	1604	CĠĠĠŦĀĠĠĀŤ	††dc††AA†ddc†dA	\rdraktakgattgga	ĊŦŦĊĊŦĠŦĀĊĠŦ	'ÀĠĠĊÀĊĊŢ	1663
Query	551	TACTCTCTGG	GGCATTATCAGATTT 	TAATAAATGAATAAA	TAAATGGTAttt	tttttAAA	610
Sbjct	1664	TACTCTCTGG	ĠĠĊÀŦŦÀŦĊĀĠÀŦŦŦ	rtaataaatgaataaa	TAAATGGTATT	ידידידידאא <sup></sup>	1723
Query	611	TGTCAGCTCT	TCCATAATTCAGTCT	AGATAGGAGATTATT	TAACTGAAGATC	TCTTGGTG	670
Sbjct	1724	TĠTĊAĠĊTĊT	tccataattcagtct	'AGATAGGAGACTATT	TAACTGAAGA	-tcttggtg	1781
Query	671	AGTGTCAttt	ttttttctttcttt	ttttttttttttt	ggttttttAAGA	CAGGGTTT	730
Sbjct	1782	AGTGTCATTT.	ΑΤΤΤΤΤΤΤ	ילכ–-דידידידידידידידידי	ĠĠ甘甘甘甘甘CÀĀĠĀ	ĊAĠĠĠŦŦŦ	1836

Query	731	CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA	790
Sbjct	1837	ctctgtgtagccctggctgtcctagaactctgtagactgggctggtctcgaactcagaga	1896
Query	791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCACCAGCTTGATGTGTGTC	850
Sbjct	1897	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTTCACCACCT-CCCAGCTTGATGTGTGTC	1953
Query	851	ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	910
Sbjct	1954	ATTTAAAACCACTGTTTAATAATCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	2013
Query	911	TTGTGGCACCCAGTGACATC-ttttttAATCAAGTGGACACACTTTTGATGTATTTCTC	969
Sbjct	2014	TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTC	2073
Query	970	AGTTACAAAGCTGACtttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTA	1029
Sbjct	2074	AGTTACAAAGCTGACTTTTTTCATGAAGGGAATAATGGCCAAGTACTCAAATCTACCTG	2133
Query	1030	AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAA-CAAAAC	1087
Sbjct	2134	AGGTACACTTTTACACCTCATCTTCTATTTCTTCCCTCTCTTCT	2193
Query	1088	AAAAC 1092	
Sbjct	2194	AAAAC 2198	

PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA

Sequence ID: **XM\_021172472.2** Length: 2297 Number of Matches: 1 Range 1: 1145 to 2159

Score		Expect	Identities	Gaps	Strand	Frame	
1576 bits	s(853)	0.0()	970/1025(95%)	13/1025(1%)	Plus/Plus		_
Query	71	GTGGTGCCATT	GGAATGTCAGCATTGCT	TTGAGTGTCATGCTC	GAGGGATGGTC	CTGACAGT	130
Sbjct	1145	GTGGTGCCATT	TTGAATGTCAGCATTGCT	TGAGTGTCATGCT		TGACAGT	1204
Query	131	AAACAGCGGGA	AAGACACCAGGAGCATTO	TAATCGCTTGGTT	AATTGTCCGAC	ATTGGTCC	190
Sbjct	1205	AAACAGCGGG	AAGGCACCGGGAGCATTC	TAATCTCTTGGTT	AATTGTCCGAC	ATTGGTCC	1264
Query	191	AGGAACAACTT	GTCTTTTCAGCCGGCTG	SACCTGCAGCCTGTA	ACAGCTCTGAA	GCATCTTT	250
Sbjct	1265	AGGAACAATTT	rGTCTTTTCAGCCGGCTC	SACCTGCAGCCTGT	ACAGCTCCGAA	GCATCTTT	1324
Query	251	AAATACGATAG	GAAAATAAGTTACTCAAG	BAAGCTGGTCTGTGT	CCTTTTGCCT	FAGTCCAT	310
Sbjct	1325	AAATACGATAC	SAAAATAAGCTACTCAAG	SAAACTGGTCTGCG	CCTTTTGCCT'	TAATCCAT	1384
Query	311	GCATACTCATT	TAAGGaaaaaaaGTACCA	ATTGTGCTAAACGCT	TACTGAGACTA	ACCAGGAA	370
Sbjct	1385	GCATACTCATT	TAAGGAAAAAAAGTACCA	ATTGTGCTTAGCGC	TACTGAGACTA	ACCAGGAA	1444
Query	371	ACCCTAAAGAT	GAAGATGTTCCTGTCC	CCGGAGCGGCTGGCT	CCACCGCAGT	GCTGGGGA	430
Sbjct	1445	ACCCTAAAGAT	rgaagatgeteeegttee	CCGGAGTGGCCGGC	rgcacagcagt	GCTGGGGA	1504
Query	431	GTTGCAGGACT	TTCATTCAAATAGGAATA	ATCAGTCCAAGCAG	GCTGATACGTG	AGTGGCAG	490
Sbjct	1505	GCTGCAGGACT	TTCATTCAGATAGGAGTA	ATCAGTCCAAGCAG	GCTGATACGTG	AGTGGCAG	1564
Query	491	TGGATAGGAT	TTGCTTAATGGCTGATG	TAATAAGATTGTACT	TTCCTATACAG	AGGCACCT	550
Sbjct	1565	CGGGTAGGATT	rtgcttaatggctgatgi	rAATAAGATTGGAC	TTCCTGTACGT	AGGCACCT	1624
Query	551	TACTCTCTGGC	GCATTATCAGATTTTA <i>F</i>	ATAAATGAATAAATA	AAATGGTAttt	ttttt <b>aaa</b>	610
Sbjct	1625	TACTCTCTGGC	GCATTATCAGATTTTA	ATAAATGAATAAAT	AAATGGTATTT	TTTTTAAA	1684
Query	611	TGTCAGCTCTT	CCATAATTCAGTCTAGA	ATAGGAGATTATTTA	AACTGAAGATC	PCTTGGTG	670
Sbjct	1685	TGTCAGCTCT	CCATAATTCAGTCTAGA	ATAGGAGACTATTT	AACTGAAGA'	rcttggtg	1742
Query	671	AGTGTCAttt	tttttctttcttttt	ttttttttttg	gttttttAAGA	CAGGGTTT	730
Sbjct	1743	AGTGTCATTT	\\\\_\\_\_\\_\_\_\_	╌╾╅╅╅╅╅╅╅╅╅╅╅	GTTTTTCAAGA	CAGGGTTT	1797
Query	731	CTCTGTGTAGO	CCTGGCTGTCCTGGAAC	CTCTGTAGACTGGG	CTGGCCTCGAA	CTCAGAGA	790
Sbjct	1798	CTCTGTGTAGO	CCTGGCTGTCCTAGAAC	CTCTGTAGACTGGG(	CTGGTCTCGAA	CTCAGAGA	1857

Query	791	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC	850
Sbjct	1858	TCTGCCTGCCCTTGCTGGGATCAGAGGTGTTCACCACCT-CCCAGCTTGATGTGTGTC	1914
Query	851	ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	910
Sbjct	1915	ATTTAAAACCACTGTTTAATAATCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC	1974
Query	911	TTGTGGCACCCAGTGACATC-tttttttAATCAAGTGGACACACTTTTGATGTATTTCTC	969
Sbjct	1975	TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTC	2034
Query	970	AGTTACAAAGCTGACtttttttaatgaagggaataattgccaagtacttaaatctaccta	1029
Sbjct	2035	AGTTACAAAGCTGACTTTTTTTCATGAAGGGAATAATGGCCAAGTACTCAAATCTACCTG	2094
Query	1030	AGGTACAC-TTTAGACCTCATCTTCTATTTCTTCCCTCTCTTCTGCAAATGAA-CAAAAC	1087
Sbjct	2095	AGGTACACTTTTACACCTCATCTTCTATTTCTTCCCTCTCTCTGCAAATAAAACAAAAC	2154
Query	1088	AAAAC 1092	
Sbjct	2155	AAAAC 2159	

#### **Taxonomy**

## Reports

### Lineage

Organism	Blast Name	Score	Number of Hits	Description
<u>Muroidea</u>	rodents		<u>101</u>	
. <u>Murinae</u>	<u>rodents</u>		<u>96</u>	
<u>Mus</u>	<u>rodents</u>		<u>92</u>	
<u>Mus</u>	rodents		<u>89</u>	
Mus musculus	rodents	1858	<u>86</u>	Mus musculus hits
Mus caroli	rodents	1576	<u>3</u>	Mus caroli hits
<u>Mus pahari</u>	<u>rodents</u>	1103	<u>3</u>	Mus pahari hits
Rattus norvegicus	<u>rodents</u>	749	<u>4</u>	Rattus norvegicus hits
Mesocricetus auratus	<u>rodents</u>	424	<u>1</u>	Mesocricetus auratus hits
.Cricetulus griseus	<u>rodents</u>	396	<u>4</u>	Cricetulus griseus hits

## • Organism

Description	Score	E value	Accession
Mus musculus (house mouse) [rodents ]			
Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1858	0.0	AK154309
PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1740	0.0	XM_006510253
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic	1740	0.0	JN961338
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgu; transgenic	1740	0.0	JN951773
Mus musculus sterol-C5-desaturase (Sc5d), mRNA	1740	0.0	NM_172769
Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence	1740	0.0	AC160051

Description	Score	E value	Accession
Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1740	0.0	AK077670
Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1740	0.0	AK043825
Mus musculus C5D mRNA for sterol-C5-desaturase, complete cds	979	0.0	AB016248
Mus musculus sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), mRNA (cDNA clone MGC:37898 IMAGE:5101986), complete cds	977	0.0	BC024132
Mus musculus BAC clone RP23-346J12 from chromosome 6, complete sequence	702	0.0	AC122333
Mus musculus predicted gene, 31520 (Gm31520), non-coding RNA	678	0.0	NR_136927
Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830041l17 product:weakly similar to STEROL C5-DESATURASE [Rattus norvegicus], full insert sequence	678	0.0	AK052921
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330029P19 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	311	5e-80	AK165139
Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone: C730048E03 product: unclassifiable, full insert sequence	292	2e-74	AK050439
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Cd3eap:tm1a(KOMP)Wtsi; transgenic	185	3e-42	JN957866
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ercc1:tm1a(KOMP)Wtsi tm2a(KOMP)Wtsi; transgenic	185	3e-42	<u>JN955142</u>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Cd3eap:tm1e(KOMP)Wtsi; transgenic	185	3e-42	JN949926
Mus musculus CD3E antigen, epsilon polypeptide associated protein (Cd3eap), mRNA	185	3e-42	NM_145822
Mus musculus chromosome 7, clone RP23-457C1, complete sequence	185	3e-42	AC118017
Mus musculus BAC clone RP23-152A3 from chromosome 9, complete sequence	185	3e-42	AC159821
Mus musculus BAC clone RP23-85B15 from chromosome 7, complete sequence	185	3e-42	AC148988
Mus musculus BAC clone RP23-135K11 from chromosome 8, complete sequence	183	1e-41	AC163625
Mus musculus strain C57BL/6J chromosome 8 clone rp23-340n2, complete sequence	183	1e-41	AC093451
Mus musculus chromosome 12, clone RP24-276C17, complete sequence	182	4e-41	AC115037
Mus musculus BAC clone RP24-140F3 from 12, complete sequence	182	4e-41	AC117240
Mus musculus BAC clone RP23-322K1 from chromosome 14, complete sequence	180	1e-40	AC125180
Mus musculus BAC clone RP23-240E9 from chromosome 9, complete sequence	180	1e-40	AC160392
<u>Mus musculus CD3E antigen, epsilon polypeptide associated protein, mRNA (cDNA clone MGC:78047 IMAGE:6478245), complete cds</u>	180	1e-40	BC071199
Mus musculus BAC clone RP23-358C4 from chromosome 9, complete sequence	178	5e-40	AC183268
Mus musculus BAC clone RP23-408l18 from chromosome 9, complete sequence	178	5e-40	AC153009
Mouse DNA sequence from clone RP23-253E9 on chromosome 11, complete sequence	178	5e-40	AL591113
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X8, mRNA	176	2e-39	XM_030252585
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X7, mRNA	176	2e-39	XM_030252584
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X6, mRNA	176	2e-39	XM_017319548
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X5, mRNA	176	2e-39	XM_006501389
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X4, mRNA	176	2e-39	XM 017319547

Description	Score	E value	Accession
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X3, mRNA	176	2e-39	XM_017319546
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X2, mRNA	176	2e-39	XM_006501386
PREDICTED: Mus musculus OTU domain containing 7B (Otud7b), transcript variant X1, mRNA	176	2e-39	XM_006501385
<u>Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Defb22:tm1a(KOMP)Wtsi; transgenic</u>	176	2e-39	JN963878
Mus musculus targeted deletion, lacZ-tagged mutant allele Sf3b4:tm1(KOMP)Ucd; transgenic	176	2e-39	JN960976
<u>Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Defb26:tm1a(KOMP)Wtsi; transgenic</u>	176	2e-39	JN959925
<u>Mus musculus targeted non-conditional, lacZ-tagged mutant allele</u> 9130017N09Rik:tm2e(EUCOMM)Wtsi tm1e(EUCOMM)Wtsi; transgenic	176	2e-39	JN958274
<u>Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele 9130017N09Rik:tm2a(EUCOMM)Wtsi; transgenic</u>	176	2e-39	JN958273
<u>Mus musculus targeted non-conditional, lacZ-tagged mutant allele</u> <u>Defb26:tm1e(KOMP)Wtsi; transgenic</u>	176	2e-39	<u>JN956718</u>
<u>Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Otud7b:tm1a(EUCOMM)Wtsi; transgenic</u>	176	2e-39	JN952505
Mus musculus targeted non-conditional, lacZ-tagged mutant allele <u>Defb22:tm1e(KOMP)Wtsi; transgenic</u>	176	2e-39	JN948829
Mus musculus BAC clone RP23-13B8 from chromosome 10, complete sequence	176	2e-39	AC151846
Mus musculus chromosome 15, clone RP23-195l24, complete sequence	176	2e-39	AC161812
Mus musculus chromosome 1, clone RP24-400M20, complete sequence	176	2e-39	AC116853
Mus musculus BAC clone RP24-389C22 from chromosome 10, complete sequence	176	2e-39	AC124407
Mus musculus chromosome 15, clone RP24-366J14, complete sequence	176	2e-39	AC163018
Mus musculus chromosome 2 clone RP23-286D16, complete sequence	176	2e-39	AC019153
Mouse DNA sequence from clone RP23-332C5 on chromosome 11, complete sequence	176	2e-39	AL645738
Mus musculus OTU domain containing 7B (Otud7b), transcript variant 1, mRNA	176	2e-39	NM_001025613
Mus musculus OTU domain containing 7B (Otud7b), transcript variant 2, mRNA	176	2e-39	NM_001025614
Mus musculus BAC clone RP23-138K22 from 9, complete sequence	176	2e-39	AC140409
Mus musculus BAC clone RP24-201C14 from 3, complete sequence	176	2e-39	AC125099
Mouse DNA sequence from clone RP23-453K8 on chromosome 2, complete sequence	176	2e-39	AL844517
Mouse DNA sequence from clone RP23-188D9 on chromosome 2, complete sequence	176	2e-39	BX004793
Mus musculus strain C57BL/6J chromosome 3 clone rp23-261m19, complete sequence	176	2e-39	AC092094
Mouse DNA sequence from clone RP23-391H10 on chromosome 2, complete sequence	176	2e-39	AL805959
Mouse DNA sequence from clone RP23-120N11 on chromosome 4, complete sequence	176	2e-39	AL683890
Mouse DNA sequence from clone RP23-129N7 on chromosome 5, complete sequence	176	2e-39	AL513345
<u>Mus musculus FtsJ RNA methyltransferase homolog 1 (E. coli) (Ftsj1), transcript variant 2, mRNA</u>	174	6e-39	NM 001290430
Mus musculus targeted non-conditional, lacZ-tagged mutant allele <u>Ftsj1:tm1e(EUCOMM)Wtsi; transgenic</u>	174	6e-39	<u>JN961376</u>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Fbxo17:tm1e(EUCOMM)Wtsi; transgenic	174	6e-39	<u>JN957410</u>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Rnd1:tm1a(EUCOMM)Wtsi; transgenic	174	6e-39	<u>JN954778</u>

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Description	Score	E value	Accession
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Micall2:tm1e(KOMP)Wtsi; transgenic	174	6e-39	JN954776
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Hnrnpu:tm1e(EUCOMM)Wtsi; transgenic	174	6e-39	JN953467
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Micall2:tm1a(KOMP)Wtsi; transgenic	174	6e-39	JN950802
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Hnrnpu:tm1a(EUCOMM)Wtsi; transgenic	174	6e-39	JN949506
<u>Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele</u> <u>Fbxo17:tm1a(EUCOMM)Wtsi; transgenic</u>	174	6e-39	JN949490
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Rnd1:tm1e(EUCOMM)Wtsi; transgenic	174	6e-39	JN947814
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ywhaq:tm1e(EUCOMM)Hmgu; transgenic	174	6e-39	JN947747
<u>Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ywhaq:tm1a(EUCOMM)Hmgu; transgenic</u>	174	6e-39	JN947251
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ftsj1:tm1a(EUCOMM)Wtsi; transgenic	174	6e-39	JN945613
Mus musculus chromosome 1, clone RP24-252K15, complete sequence	174	6e-39	AC166710
Mus musculus BAC clone RP23-27C10 from chromosome 1, complete sequence	174	6e-39	AC125377
Mus musculus BAC clone RP23-264L8 from chromosome 14, complete sequence	174	6e-39	AC158983
Mus musculus BAC clone RP23-168E11 from chromosome 5, complete sequence	174	6e-39	AC130221
Mus musculus BAC clone RP24-505G5 from chromosome 7, complete sequence	174	6e-39	AC125372
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832403P19 product:DSCAM-interacting protein 1 homolog [Mus musculus], full insert sequence	174	6e-39	<u>AK161178</u>
Mus musculus BAC clone RP24-490B17 from chromosome 17, complete sequence	174	6e-39	AC154796
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630055M22 product:Ftsj homolog (E. coli), full insert sequence	174	6e-39	AK036313
Mus caroli (Ryukyu mouse) [rodents ]			
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA	1576	0.0	XM_029481771
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	1576	0.0	XM_021172472
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1576	0.0	XM 021172471
Mus pahari (shrew mouse) [rodents ]			
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1103	0.0	XM_021207205
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	699	0.0	XM 021207206
PREDICTED: Mus pahari lathosterol oxidase-like (LOC110334695), mRNA	579	1e-160	XM 029547953
Rattus norvegicus (Norway rat) [rodents ]			
PREDICTED: Rattus norvegicus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	749	0.0	XM_017595406
Rattus norvegicus sterol-C5-desaturase (Sc5d), mRNA	749	0.0	NM 053642
Rattus norvegicus sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like, mRNA (cDNA clone MGC:93101 IMAGE:7131154), complete cds	749	0.0	BC081704
Rattus norvegicus C5D mRNA for sterol C5-desaturase, complete cds	407	6e-109	AB052846
Mesocricetus auratus (golden hamster) [rodents ]			<del></del>
PREDICTED: Mesocricetus auratus sterol-C5-desaturase (Sc5d), mRNA	424	6e-114	XM 005069403
Cricetulus griseus (Chinese hamster) [rodents ]		•	
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	396	1e-105	XM_007651891

Description	Score	E value	Accession
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	396	1e-105	XM_003511371
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	392	2e-104	XM_027411877
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	392	2e-104	XM_027411876

### Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
<u>Muroidea</u>	<u>101</u>	6	
. <u>Murinae</u>	<u>96</u>	4	
<u>Mus</u>	<u>92</u>	3	
<u>Mus</u>	<u>89</u>	2	
Mus musculus	86	1	Mus musculus hits
Mus caroli	<u>3</u>	1	Mus caroli hits
<u>Mus pahari</u>	<u>3</u>	1	Mus pahari hits
Rattus norvegicus	<u>4</u>	1	Rattus norvegicus hits
. <u>Cricetinae</u>	<u>5</u>	2	
Mesocricetus auratus	<u>1</u>	1	Mesocricetus auratus hits
Cricetulus griseus	<u>4</u>	1	<u>Cricetulus griseus hits</u>

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